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<first sequence: ss.AR350065 (length = 1381)
<second sequence: ss.DNA57033 (length = 2056)

<1362 matches in an overlap of 1381: 98.62 percent similarity
<gaps in first sequence: 2 (3 bases), gaps in second sequence: 3 (3 bases)
<score: 4040 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)
<endgaps not penalized

GenBank (Release 143, aug 2004)[Sep 10 16:50:21 2004]:

AR350065    Sequence 1 from patent US 6586228. 1381 bp,
            DNA, linear, PAT 17-AUG-2003
ACCESSION   AR350065
VERSION     AR350065.1  GI:33751016
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1381)
  AUTHORS   Parham,C.L., Moore,K.W. and Murgolo,N.J.
  TITLE     Polynucleotides encoding DIRS1
  JOURNAL   Patent: US 6586228-A 1 01-JUL-2003;
FEATURES             Location/Qualifiers
     source          1..1381
                     /organism="unknown"
                     /mol_type="genomic DNA"
BASE COUNT
ORIGIN


ss.DNA57033   AAAGTTACATTTTCTCTGGAACTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTT
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ss.AR350065                                                          TCG
                                                                     * *
ss.DNA57033   TGGGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAG
                     70        80        90       100       110       120

                   10        20        30        40        50        60
ss.AR350065   ACCCACGC-GTCCGCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAG
              * * *  * * *  ********************************************
ss.DNA57033   AACAATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAG
              130       140       150       160       170       180

                  70        80        90       100       110       120
ss.AR350065   ATGGCTGAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACTGA
              ************************************************************
ss.DNA57033   ATGGCTGAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACTGA
              190       200       210       220       230       240

                 130       140       150       160       170       180
ss.AR350065   GTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATG
              ************************************************************
ss.DNA57033   GTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATG
              250       260       270       280       290       300
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                190        200        210        220        230        240
ss.AR350065     TGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCC
                ************************************************************
ss.DNA57033     TGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCC
                  310        320        330        340        350        360

                250        260        270        280        290        300
ss.AR350065     CCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTG
                ************************************************************
ss.DNA57033     CCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTG
                  370        380        390        400        410        420

                310        320        330        340        350        360
ss.AR350065     ATCGCGCCTGGAGAAACAGTGTACTATTCTGTCGAATACCAGGGGGAGTACGAGAGCCTG
                ************************************************************
ss.DNA57033     ATCGCGCCTGGAGAAACAGTGTACTATTCTGTCGAATACCAGGGGGAGTACGAGAGCCTG
                  430        440        450        460        470        480

                370        380        390        400        410        420
ss.AR350065     TACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGT
                ************************************************************
ss.DNA57033     TACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGT
                  490        500        510        520        530        540

                430        440        450        460        470        480
ss.AR350065     GATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTG
                ************************************************************
ss.DNA57033     GATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTG
                  550        560        570        580        590        600

                490        500        510        520        530        540
ss.AR350065     GGCTCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATC
                ************************************************************
ss.DNA57033     GGCTCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATC
                  610        620        630        640        650        660

                550        560        570        580        590        600
ss.AR350065     CTTACCCGACCTGGGATGGAGATCXCCAAAXATGGCTTCCACCTGGTTATTGAGCTGGAG
                ************************ ***** ******************************
ss.DNA57033     CTTACCCGACCTGGGATGGAGATCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAG
                  670        680        690        700        710        720

                610        620        630        640        650        660
ss.AR350065     GACCTGGGGCCCCAGTTTGAGTTCCTTGTGGCCTACTGGASGAGGGAGCCTGGTGCCGAG
                ************************************************************
ss.DNA57033     GACCTGGGGCCCCAGTTTGAGTTCCTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAG
                  730        740        750        760        770        780

                670        680        690        700        710        720
ss.AR350065     GAACATGTCAAAATGGTGAGGAGTGGGGGTATTCCAGTGCACCTAGAAACCATGGAGCCA
                ************************************************************
ss.DNA57033     GAACATGTCAAAATGGTGAGGAGTGGGGGTATTCCAGTGCACCTAGAAACCATGGAGCCA
                  790        800        810        820        830        840

                730        740        750        760        770        780
ss.AR350065     GGGGCTGCATACTGTGTGAAGGCCCAGACATTCGTGAAGGCCATTGGGARGTACAGCGCC
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ss.DNA57033    GGGGCTGCATACTGTGTGAAGGCCCAGACATTCGTGAAGGCCATTGGGAGGTACAGCGCC
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                790       800       810       820       830       840
ss.AR350065    TTCAGCCAGACAGAATGTGTGGARGTGCAAGGAGAGGCCATTCCCCTGGTACTGGCCCTG
               ************************************************************
ss.DNA57033    TTCAGCCAGACAGAATGTGTGGAGGTGCAAGGAGAGGCCATTCCCCTGGTACTGGCCCTG
                     910       920       930       940       950       960

                850       860       870       880       890       900
ss.AR350065    TTTGCCTTTGTTGGCTTCATGCTGATCCTTGTGGTCGTGCCACTGTTCGTCTGGAAAATG
               ************************************************************
ss.DNA57033    TTTGCCTTTGTTGGCTTCATGCTGATCCTTGTGGTCGTGCCACTGTTCGTCTGGAAAATG
                     970       980       990      1000      1010      1020

                910       920       930       940       950       960
ss.AR350065    GGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGGTGGTCCTCCCAGACACCTTGAAAATA
               ************************************************************
ss.DNA57033    GGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGGTGGTCCTCCCAGACACCTTGAAAATA
                    1030      1040      1050      1060      1070      1080

                970       980       990      1000      1010      1020
ss.AR350065    ACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGGGAGGAGGTGGATGCCTGTGCCACG
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ss.DNA57033    ACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGGGAGGAGGTGGATGCCTGTGCCACG
                    1090      1100      1110      1120      1130      1140

               1030      1040      1050      1060      1070      1080
ss.AR350065    GCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGATCTCATAGGTTTGCGGAAGGGCC
               ************************************************************
ss.DNA57033    GCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGATCTCATAGGTTTGCGGAAGGGCC
                    1150      1160      1170      1180      1190      1200

               1090      1100      1110      1120      1130      1140
ss.AR350065    CAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACCATGAGGGGACAAGTTGTGTT
               ************************************************************
ss.DNA57033    CAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACCATGAGGGGACAAGTTGTGTT
                    1210      1220      1230      1240      1250      1260

               1150      1160      1170      1180      1190      1200
ss.AR350065    TCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGAGCCTGTTGTCTACAAGTC
               ************************************************************
ss.DNA57033    TCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGAGCCTGTTGTCTACAAGTC
                    1270      1280      1290      1300      1310      1320

               1210      1220      1230      1240      1250      1260
ss.AR350065    TAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCKAACAGAACAAYTGACTGAGGYTAKRG
               ****************************************** ************* ***
ss.DNA57033    TAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAAC-ACTGACTGAGGCT-TAG
                    1330      1340      1350      1360      1370

               1270      1280      1290      1300      1310      1320
ss.AR350065    GGGWTGTGACCTCTAGACTKTGGGSTKSCAYTTGCWTGGYTGAGCAACCCTGGGAAAAGT
               ******************* ************** ************************
ss.DNA57033    GGGATGTGACCTCTAGACTGGGGGCTGCCACTTGC-TGGCTGAGCAACCCTGGGAAAAGT
          1380      1390      1400      1410      1420      1430
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                    1330       1340       1350       1360        1370       1380
ss.AR350065   GACTTCATCCCTTXGGTCCXAAGTTTTCTCATCTGTAATGGGGGA--TXCCTACAAAACT
              ************** ***** ************************  * ****** * **
ss.DNA57033   GACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACCTACACACCT
             1440       1450       1460       1470       1480       1490


ss.AR350065   G
              *
ss.DNA57033   GCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAATACACCC
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ss.DNA57033   AGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTCAGTGTTT
             1560       1570       1580       1590       1600       1610

ss.DNA57033   CTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGTGGC
             1620       1630       1640       1650       1660       1670

ss.DNA57033   TTGGAGAGCCCACTTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGGT
             1680       1690       1700       1710       1720       1730

ss.DNA57033   GTTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAG
             1740       1750       1760       1770       1780       1790

ss.DNA57033   TAGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGG
             1800       1810       1820       1830       1840       1850

ss.DNA57033   ATCCATGAACTACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATG
             1860       1870       1880       1890       1900       1910

ss.DNA57033   TATGTGTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTTGTGCTCC
             1920       1930       1940       1950       1960       1970

ss.DNA57033   TTTTTTCTGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGC
             1980       1990       2000       2010       2020       2030

ss.DNA57033   GGTAAAAAAAAAAAAAAA
             2040       2050
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